

SEQUENCE LISTING

<110> Staskawicz, et al.

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agc Ser	ctg Leu 105	caa Gln	caa Gln	gta Val	gca Ala	gag Glu 110	gac Asp	atg Met	gat Asp	cat His	atc Ile	tgg Trp 115	aaa Lys	gag Glu	tcg Ser	449
aca Thr 120	aag Lys	atc Ile	caa Gln	gat Asp	aaa Lys 125	gga Gly	aaa Lys	caa Gln	gta Val	tca Ser 130	aag Lys	gaa Glu	tca Ser	ttg Leu	gtt Val 135	497
cat His	gat Asp	ttt Phe	tca Ser 140	agt Ser	tca Ser	aca Thr	aac Asn	gat Asp	att Ile 145	ttg Leu	aag Lys	gtt Val	aag Lys	aac Asn 150	aat Asn	545
atg Met	gtt Val	gga Gly 155	cgt Arg	gat Asp	gat Asp	caa Gln	agg Arg	aaa Lys 160	cag Gln	ttg Leu	tta Leu	gaa Glu	gat Asp 165	ctg Leu	act Thr	593
aga Arg	agc Ser	tac Tyr 170	tct Ser	ggg Gly	gaa Glu	ccc Pro	aaa Lys 175	gtc Val	atc Ile	ccg Pro	att Ile	gtc Val 180	ggg Gly	atg Met	gga Gly	641
ggc Gly	ata Ile 185	ggt Gly	aaa Lys	aca Thr	acc Thr	tta Leu 190	gca Ala	aaa Lys	gaa Glu	gtt Val	tac Tyr 195	aat Asn	gat Asp	gaa Glu	tca Ser	689
att Ile 200	cta Leu	tgc Cys	cgt Arg	ttt Phe 205	gat Asp	gtt Val	cat His	gcc Ala	tgg Trp	gct Ala 210	acc Thr	ata Ile	tct Ser	caa Gln	cag Gln 215	737
cac His	aac Asn	aaa Lys	aag Lys	gaa Glu 220	att Ile	ttg Leu	ctg Leu	ggc Gly	ctt Leu 225	ctg Leu	cat His	tcc Ser	aca Thr	atc Ile 230	aaa Lys	785
atg Met	gat Asp	gac Asp	agg Arg 235	gtt Val	aag Lys	atg Met	att Ile	ggt Gly 240	gaa Glu	gca Ala	gag Glu	cta Leu	gca Ala	gac Asp 245	atg Met	833
tta Leu	cag Gln 250	aaa Lys	agt Ser	tta Leu	aag Lys	aga Arg	aag Lys 255	agg Arg	tac Tyr	tta Leu	att Ile	gtc Val 260	ttg Leu	gat Asp	gat Asp	881
atc Ile	tgg Trp 265	agt Ser	tgt Cys	gaa Glu	gtg Val	tgg Trp 270	gat Asp	ggc Gly	gtg Val	aga Arg	cga Arg 275	tgc Cys	ttt Phe	cca Pro	act Thr	929

gaa gac aat gca ggg agt cga ata ctg ttg act acc cgt aat gat gaa Glu Asp Asn Ala Gly Ser Arg Ile Leu Leu Thr Thr Arg Asn Asp Glu 280 285 290 295	977
gta gct tgt tat gct ggt gta gag aat ttt tct ttg cgg atg agc ttc Val Ala Cys Tyr Ala Gly Val Glu Asn Phe Ser Leu Arg Met Ser Phe 300 305 310	1025
atg gat caa gat gag agt tgg agt ctt ttc aaa agt gca gca ttt tca Met Asp Gln Asp Glu Ser Trp Ser Leu Phe Lys Ser Ala Ala Phe Ser 315 320 325	1073
agt gaa gca tta cca tat gag ttc gag act gtt gga aag caa atc gca Ser Glu Ala Leu Pro Tyr Glu Phe Glu Thr Val Gly Lys Gln Ile Ala 330 335 340	1121
gat gaa tgt cac ggg tta cca cta act att gtc gtg gtt gca ggg ctt Asp Glu Cys His Gly Leu Pro Leu Thr Ile Val Val Val Ala Gly Leu 345 350 355	1169
ctc aaa tct aaa agg aca ata gaa gat tgg aaa act gtt gct aaa gat Leu Lys Ser Lys Arg Thr Ile Glu Asp Trp Lys Thr Val Ala Lys Asp 360 365 370 375	1217
gtc aag tca ttc gtc aca aat gat cct gat gaa cga tgt tca cgt gtg Val Lys Ser Phe Val Thr Asn Asp Pro Asp Glu Arg Cys Ser Arg Val 380 385 390	1265
ctt ggg ttg agt tac gat cac ttg aca agc gat cta aaa aca tgt ctt Leu Gly Leu Ser Tyr Asp His Leu Thr Ser Asp Leu Lys Thr Cys Leu 395 400 405	1313
ctg cat ttc gga att ttt cca gaa gac agt gat att cca gtg aag aat Leu His Phe Gly Ile Phe Pro Glu Asp Ser Asp Ile Pro Val Lys Asn 410 415 420	1361
ttg atg aga tca tgg atg gct gag ggg ttc ctg aag ttg gaa aat gat Leu Met Arg Ser Trp Met Ala Glu Gly Phe Leu Lys Leu Glu Asn Asp 425 430 435	1409
ttg gaa gga gag gtt gag aag tgt ttg caa gag ctt gtc gat aga tgt Leu Glu Gly Glu Val Glu Lys Cys Leu Gln Glu Leu Val Asp Arg Cys 440 445 450 455	1457
cta gtc ctc gtc agc aag aga agt cga gat gga aca aaa att aga tca Leu Val Leu Val Ser Lys Arg Ser Arg Asp Gly Thr Lys Ile Arg Ser 460 465 470	1505
tgt aag gtt cat gat cta ata tat gac ctg tgc gtg aga gaa gtt caa Cys Lys Val His Asp Leu Ile Tyr Asp Leu Cys Val Arg Glu Val Gln 475 480 485	1553
agg gag aac att ttt atc atg aac gac att gtt ctt gac gta tca tat Arg Glu Asn Ile Phe Ile Met Asn Asp Ile Val Leu Asp Val Ser Tyr 490 495 500	1601
cca gaa tgt tca tat ctc tgt atg tat aaa atg cag ccc ttt aag cgc Pro Glu Cys Ser Tyr Leu Cys Met Tyr Lys Met Gln Pro Phe Lys Arg 505 510 515	1649
gtg act ggt gat gaa att aat tat tgt ccc tat ggt ctt tat agg gct	1697

Val Thr Gly Asp Glu Ile Asn Tyr Cys Pro Tyr Gly Leu Tyr Arg Ala	520	525	530	535	
ctt ctt acc cct gta aat cgt cag ttg aga gat cat gac aac aac aat	1745				
Leu Leu Thr Pro Val Asn Arg Gln Leu Arg Asp His Asp Asn Asn Asn		540	545	550	
ctt ttg aaa cga acc cat tct gtt ttc tct ttt cat ctt gag cct tta	1793				
Leu Leu Lys Arg Thr His Ser Val Phe Ser Phe His Leu Glu Pro Leu		555	560	565	
tat tat gtt ctc aaa tca gag gtt gtt cat ttc aaa tta ctc aaa gtc	1841				
Tyr Tyr Val Leu Lys Ser Glu Val Val His Phe Lys Leu Leu Lys Val		570	575	580	
ttg gag ctg aga cac aga cag att gat ggt ttc cct cga gag ata cta	1889				
Leu Glu Leu Arg His Arg Gln Ile Asp Gly Phe Pro Arg Glu Ile Leu		585	590	595	
agc ctc atc tgg ttg agg tac cta tca ttg ttc agc tat ggg aat ttc	1937				
Ser Leu Ile Trp Leu Arg Tyr Leu Ser Leu Phe Ser Tyr Gly Asn Phe		600	605	610	615
gat gta cct cca gaa att tgc agg tta tgg aat ctg cag aca ttc att	1985				
Asp Val Pro Pro Glu Ile Cys Arg Leu Trp Asn Leu Gln Thr Phe Ile		620	625	630	
gtt caa cgg ttt cga tca gat ata ata att ttt gct gag gaa att tgg	2033				
Val Gln Arg Phe Arg Ser Asp Ile Ile Ile Phe Ala Glu Glu Ile Trp		635	640	645	
gaa cta atg caa tta agg cat ctt aaa ctg ccc aga ttt tat ttg cca	2081				
Glu Leu Met Gln Leu Arg His Leu Lys Leu Pro Arg Phe Tyr Leu Pro		650	655	660	
gat tgc cca agt gga tct gtt gac aaa gga agg cac ttg gat ttt tca	2129				
Asp Cys Pro Ser Gly Ser Val Asp Lys Gly Arg His Leu Asp Phe Ser		665	670	675	
aac tta caa act att tct tac ttg tct cca cgt tgt tgc acg aag gag	2177				
Asn Leu Gln Thr Ile Ser Tyr Leu Ser Pro Arg Cys Cys Thr Lys Glu		680	685	690	695
gtt att atg ggg att cag aat gtc aaa aaa tta gga atc agt gga aat	2225				
Val Ile Met Gly Ile Gln Asn Val Lys Lys Leu Gly Ile Ser Gly Asn		700	705	710	
aag gat gac tat aaa agt ttt cgg gac tct ggg ctt ccc aac aat ctt	2273				
Lys Asp Asp Tyr Lys Ser Phe Arg Asp Ser Gly Leu Pro Asn Asn Leu		715	720	725	
gtc tat ctg cag caa ctt gaa ata ttg agt ctt ata tct gtt gat tat	2321				
Val Tyr Leu Gln Gln Leu Glu Ile Leu Ser Leu Ile Ser Val Asp Tyr		730	735	740	
agc ctt ttg cca gtg atc att tca agt gca aaa gct ttt cca gca acg	2369				
Ser Leu Leu Pro Val Ile Ile Ser Ser Ala Lys Ala Phe Pro Ala Thr		745	750	755	
ctc aag aag ttg aag ttg gaa aga act tat cta agc tgg tca tac ttg	2417				
Leu Lys Lys Leu Lys Leu Glu Arg Thr Tyr Leu Ser Trp Ser Tyr Leu					

760	765	770	775	
gac atc ata gct gag ttg cct aac ctt gag gtg ctg aag ctg atg gat				2465
Asp Ile Ile Ala Glu Leu Pro Asn Leu Glu Val Leu Lys Leu Met Asp				
	780	785	790	
gac gct tgt tgt ggt gaa gaa tgg cat cca att gtt atg gga ttt aat				2513
Asp Ala Cys Cys Gly Glu Glu Trp His Pro Ile Val Met Gly Phe Asn				
	795	800	805	
cga ttg aag ctt ttg cta att aaa tat agt ttt ctc aag ttc tgg aaa				2561
Arg Leu Lys Leu Leu Leu Ile Lys Tyr Ser Phe Leu Lys Phe Trp Lys				
	810	815	820	
gcc aca aat gac aat ttt cct gtc ctt gag cgc ctc atg att aga agt				2609
Ala Thr Asn Asp Asn Phe Pro Val Leu Glu Arg Leu Met Ile Arg Ser				
	825	830	835	
tgc aaa aat ttg aaa gag ata ccc att gag ttt gca gat ata cac aca				2657
Cys Lys Asn Leu Lys Glu Ile Pro Ile Glu Phe Ala Asp Ile His Thr				
	840	845	850	855
cta cag ctg att gag tta aga gag tgt cct ccc aaa ctt ggg gaa tct				2705
Leu Gln Leu Ile Glu Leu Arg Glu Cys Pro Pro Lys Leu Gly Glu Ser				
	860	865	870	
gct gca cga att cag aaa gaa caa gaa gac ctc gga aac aac cct gtg				2753
Ala Ala Arg Ile Gln Lys Glu Gln Glu Asp Leu Gly Asn Asn Pro Val				
	875	880	885	
gat gtt cgt atc tca aat cca ttg aag gag agt gat tct gat tca gaa				2801
Asp Val Arg Ile Ser Asn Pro Leu Lys Glu Ser Asp Ser Asp Ser Glu				
	890	895	900	
gaa cat tag gaaaggatct caaggccaga aggattgaac tcttgggatt				2850
Glu His				
	905			
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tccaaggaga tgtgatatct tttgtgttgt aacatatattt tgagttgtac tgattccctt				2970
cttcccttct ctttttatgt aactttacta attcaacttc aagtactagc agaccacatg				3030
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aaaaaaaa				3099
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Leu Thr Phe Asn Ser Pro Met Gln Ser Leu Ser Cys Asp His Arg Glu				
20	25	30		

[illegible]

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35 40 45																
aag aac ttt gag aaa aac aat gtt ttt ggg gaa atg acg gat ttt gaa Lys Asn Phe Glu Lys Asn Asn Val Phe Gly Glu Met Thr Asp Phe Glu																192
50 55 60																
gta gag gta aga gaa gtt gca agt gct gct gaa tac aca att caa ctg Val Glu Val Arg Glu Val Ala Ser Ala Ala Glu Tyr Thr Ile Gln Leu																240
65 70 75 80																
aga cta aca gga act gta ctg gga gaa aat aaa agc cag aaa aaa aag Arg Leu Thr Gly Thr Val Leu Gly Glu Asn Lys Ser Gln Lys Lys Lys																288
85 90 95																
gcg cgt cga agg ttt cgt caa agc ctg caa caa gta gca gag gac atg Ala Arg Arg Arg Phe Arg Gln Ser Leu Gln Gln Val Ala Glu Asp Met																336
100 105 110																
gat cat atc tgg aaa gag tcg aca aag atc caa gat aaa gga aaa caa Asp His Ile Trp Lys Glu Ser Thr Lys Ile Gln Asp Lys Gly Lys Gln																384
115 120 125																
gta tca aag gaa tca ttg gtt cat gat ttt tca agt tca aca aac gat Val Ser Lys Glu Ser Leu Val His Asp Phe Ser Ser Ser Thr Asn Asp																432
130 135 140																
att ttg aag gtt aag aac aat atg gtt gga cgt gat gat caa agg aaa Ile Leu Lys Val Lys Asn Asn Met Val Gly Arg Asp Asp Gln Arg Lys																480
145 150 155 160																
cag ttg tta gaa gat ctg act aga agc tac tct ggg gaa ccc aaa gtc Gln Leu Leu Glu Asp Leu Thr Arg Ser Tyr Ser Gly Glu Pro Lys Val																528
165 170 175																
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180 185 190																
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195 200 205																
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210 215 220																
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225 230 235 240																
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245 250 255																
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260 265 270																

gtg aga cga tgc ttt cca act gaa gac aat gca ggg agt cga ata ctg	864
Val Arg Arg Cys Phe Pro Thr Glu Asp Asn Ala Gly Ser Arg Ile Leu	
275 280 285	
ttg act acc cgt aat gat gaa gta gct tgt tat gct ggt gta gag aat	912
Leu Thr Thr Arg Asn Asp Glu Val Ala Cys Tyr Ala Gly Val Glu Asn	
290 295 300	
ttt tct ttg cgg atg agc ttc atg gat caa gat gag agt tgg agt ctt	960
Phe Ser Leu Arg Met Ser Phe Met Asp Gln Asp Glu Ser Trp Ser Leu	
305 310 315 320	
ttc aaa agt gca gca ttt tca agt gaa gca tta cca tat gag ttc gag	1008
Phe Lys Ser Ala Ala Phe Ser Ser Glu Ala Leu Pro Tyr Glu Phe Glu	
325 330 335	
act gtt gga aag caa atc gca gat gaa tgt cac ggg tta cca cta act	1056
Thr Val Gly Lys Gln Ile Ala Asp Glu Cys His Gly Leu Pro Leu Thr	
340 345 350	
att gtc gtg gtt gca ggg ctt ctc aaa tct aaa agg aca ata gaa gat	1104
Ile Val Val Val Ala Gly Leu Leu Lys Ser Lys Arg Thr Ile Glu Asp	
355 360 365	
tggtg aaa act gtt gct aaa gat gtc aag tca ttc gtc aca aat gat cct	1152
Trp Lys Thr Val Ala Lys Asp Val Lys Ser Phe Val Thr Asn Asp Pro	
370 375 380	
gat gaa cga tgt tca cgt gtg ctt ggg ttg agt tac gat cac ttg aca	1200
Asp Glu Arg Cys Ser Arg Val Leu Gly Leu Ser Tyr Asp His Leu Thr	
385 390 395 400	
agc gat cta aaa aca tgt ctt ctg cat ttc gga att ttt cca gaa gac	1248
Ser Asp Leu Lys Thr Cys Leu Leu His Phe Gly Ile Phe Pro Glu Asp	
405 410 415	
agt gat att cca gtg aag aat ttg atg aga tca tgg atg gct gag ggg	1296
Ser Asp Ile Pro Val Lys Asn Leu Met Arg Ser Trp Met Ala Glu Gly	
420 425 430	
ttc ctg aag ttg gaa aat gat ttg gaa gga gag gtt gag aag tgt ttg	1344
Phe Leu Lys Leu Glu Asn Asp Leu Glu Gly Glu Val Glu Lys Cys Leu	
435 440 445	
caa gag ctt gtc gat aga tgt cta gtc ctc gtc agc aag aga agt cga	1392
Gln Glu Leu Val Asp Arg Cys Leu Val Leu Val Ser Lys Arg Ser Arg	
450 455 460	
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Asp Gly Thr Lys Ile Arg Ser Cys Lys Val His Asp Leu Ile Tyr Asp	
465 470 475 480	
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Leu Cys Val Arg Glu Val Gln Arg Glu Asn Ile Phe Ile Met Asn Asp	
485 490 495	
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Ile Val Leu Asp Val Ser Tyr Pro Glu Cys Ser Tyr Leu Cys Met Tyr	
500 505 510	
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755						760				765						
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Tyr	Leu	Ser	Trp	Ser	Tyr	Leu	Asp	Ile	Ile	Ala	Glu	Leu	Pro	Asn	Leu	
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gag	gtg	ctg	aag	ctg	atg	gat	gac	gct	tgt	tgt	ggg	gaa	gaa	tgg	cat	2400
Glu	Val	Leu	Lys	Leu	Met	Asp	Asp	Ala	Cys	Cys	Gly	Glu	Glu	Trp	His	
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Pro	Ile	Val	Met	Gly	Phe	Asn	Arg	Leu	Lys	Leu	Leu	Leu	Ile	Lys	Tyr	
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agt	ttt	ctc	aag	ttc	tgg	aaa	gcc	aca	aat	gac	aat	ttt	cct	gtc	ctt	2496
Ser	Phe	Leu	Lys	Phe	Trp	Lys	Ala	Thr	Asn	Asp	Asn	Phe	Pro	Val	Leu	
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gag	cgc	ctc	atg	att	aga	agt	tgc	aaa	aat	ttg	aaa	gag	ata	ccc	att	2544
Glu	Arg	Leu	Met	Ile	Arg	Ser	Cys	Lys	Asn	Leu	Lys	Glu	Ile	Pro	Ile	
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cct	ccc	aaa	ctt	ggg	gaa	tct	gct	gca	cga	att	cag	aaa	gaa	caa	gaa	2640
Pro	Pro	Lys	Leu	Gly	Glu	Ser	Ala	Ala	Arg	Ile	Gln	Lys	Glu	Gln	Glu	
	865				870					875					880	
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Asp	Leu	Gly	Asn	Asn	Pro	Val	Asp	Val	Arg	Ile	Ser	Asn	Pro	Leu	Lys	
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<220>

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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer 2

<400> 6

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25

<210> 7
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 3

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<210> 8
<211> 25
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer 4

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